

SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> Helicobacter vaccine

<130> Degoedesequenties

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<170> PatentIn Ver. 2.1

<210> 1

<211> 2883

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (206)..(886)

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<222> (897)..(2603)

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ttacttatat taaaaagtta ataaaaagta acgaaattag gactataatc ccattgcott 180

taaaatttaa cacaaggagt aatag gtg aaa ctc aca ccc aaa gag caa gaa 232

Val Lys Leu Thr Pro Lys Glu Gln Glu

Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile
 155 160 165

ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg 760
 Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val
 170 175 180 185

cag ttg att cct ctt ggt ggc agt aaa aaa gtg att ggc atg aac ggg 808
 Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly
 190 195 200

ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac 856
 Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp
 205 210 215

aag gcg aaa tct cac gga ttt atc aag taa ggagactccc atg aaa atg 905
 Lys Ala Lys Ser His Gly Phe Ile Lys Met Lys Met
 220 225 230

aaa aaa caa gaa tat gta aat acc tac gga ccc acc aaa ggc gat aaa 953
 Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys Gly Asp Lys
 235 240 245

gtg cgc tta gga gat acc gat ctt tgg gca gaa gta gaa cat gac tat 1001
 Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu His Asp Tyr
 250 255 260

acc acc tat ggc gaa gaa ctt aaa ttt ggc gcg ggt aaa act atc cgt 1049
 Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg
 265 270 275

gag ggt atg ggt cag agc aat agc cct gat gaa aac acc cta gat tta 1097
 Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu
 280 285 290

gtc atc act aac gcg atg att atc gac tac acc ggg att tac aaa gcc 1145
 Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala
 295 300 305 310

Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr Asp Val Gln
 455 460 465 470

gtt tgt atc cac acc gat aca gtc aat gag gca ggt tat gta gat gac 1673
 Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr Val Asp Asp
 475 480 485

acc cta aat gca atg aac ggg cgc gcc atc cat gcc tac cac att gag 1721
 Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr His Ile Glu
 490 495 500

gga gcg ggt gga gga cac tca cct gat gtt atc acc atg gca ggc gag 1769
 Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met Ala Gly Glu
 505 510 515

ctc aat att cta ccc tcc tcc acc acc ccc act att ccc tat acc att 1817
 Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile
 520 525 530

aat acg gtt gca gaa cac tta gac atg ctc atg aca tgc cac cac cta 1865
 Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys His His Leu
 535 540 545 550

gac aaa cgc atc cgc gag gat tta caa ttt tct caa agc cgt atc cgc 1913
 Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg
 555 560 565

ccc ggc tct atc gcg gct gaa gat gtg ctc cat gat atg ggt gtg atc 1961
 Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Val Ile
 570 575 580

gcg atg aca agc tcg gat tcg caa gca atg ggg cgt gca ggc gaa gtg 2009
 Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala Gly Glu Val
 585 590 595

att cct cga act tgg cag act gcg gat aag aat aaa aaa gaa ttt ggt 2057
 Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly
 600 605 610

Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val Phe Val Asp
 760 765 770

ggc aaa ctc tgc acc tct aaa ccc acc tcg caa gtg cct cta gcc cag 2585
 Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro Leu Ala Gln
 775 780 785 790

cgc tac act ttc ttc tag gcacaatgcc ccctttgggg gcaggttatt 2633
 Arg Tyr Thr Phe Phe
 795

ttaggaatct tcatcaaacg cacctgcaat cggctcttgcg tgtgcgatcg tgctgccttta 2693

aaacaacttt tcattcttta gcaatcgcca tttttaatta atttaattct tataattaat 2753

attatattat gccccctcat ttttaaagga gaattatgcg taggtctttg gtattgctat 2813

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<213> Helicobacter felis

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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
 20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45

Arg Gly Lys Lys Thr Val Ala Gln Leu Met Glu Glu Cys Met His Phe

FOET-20-14000000

50

55

60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
 210 215 220

Ile Lys
 225

<210> 3

<211> 568

FOEFO-7540000

190

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met
340 345 350

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
565

TOEFD-404000

aat tgg ccc att gaa cct gat gaa cac ttt aaa gcc ggt gaa gtg aaa 336
 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110

ttt ggc tgt gat aaa gac att gag ctc aac gcg ggt aag gaa gtt acc 384
 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125

gag ctt gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc 432
 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140

cat ttc cac ttc ttt gaa acc aac aag gca ttg aaa ttc gat cgg gaa 480
 His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160

aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc 528
 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175

att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggt 576
 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190

agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg gac 624
 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205

gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga ttc 672
 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
 210 215 220

atc aag taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aac 721
 Ile Lys Met Lys Met Lys Lys Gln Glu Tyr Val Asn
 225 230 235

acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc gat 769
 Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp

240	245	250	
ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc	817		
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu			
255	260	265	
aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc aat	865		
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn			
270	275	280	285
agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg att	913		
Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile			
290	295	300	
atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat ggc	961		
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly			
305	310	315	
aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat ggc	1009		
Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly			
320	325	330	
gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca ggg	1057		
Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly			
335	340	345	
gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac ttc	1105		
Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe			
350	355	360	365
ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca acc	1153		
Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr			
370	375	380	
atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc acc	1201		
Met Phe Gly Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr			
385	390	395	

TCF20-460660

atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa 1249
 Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu
 400 405 410

gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt 1297
 Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser
 415 420 425

aaa aaa caa ctc gta gaa caa gta gaa gcg ggc gcg att ggc ttt aaa 1345
 Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe Lys
 430 435 440 445

ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc ttg 1393
 Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu
 450 455 460

agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg 1441
 Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr
 465 470 475

gtc aat gag gca ggt tat gta gat gac acc cta aat gcg atg aac ggg 1489
 Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly
 480 485 490

cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca 1537
 Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly Gly His Ser
 495 500 505

cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc tcc 1585
 Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser
 510 515 520 525

acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac tta 1633
 Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu
 530 535 540

gac atg ctc atg acc tgc cac cac cta gac aaa cgc atc cgc gag gat 1681
 Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp

545	550	555	
ctc cag ttt tcc caa agc cgt atc cgc ccc ggc tct att gcc gct gaa			1729
Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu			
560	565	570	
gat gtg ctc cat gat att ggc gtg atc gcg atg aca agc tcg gat tcg			1777
Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser			
575	580	585	
caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa act			1825
Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr			
590	595	600	605
gca gac aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt gca			1873
Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala			
610	615	620	
gat aat gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc att			1921
Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile			
625	630	635	
aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg gaa			1969
Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu			
640	645	650	
gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gct ttc ttt ggt			2017
Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly			
655	660	665	
gta aaa ccc aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa			2065
Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu			
670	675	680	685
atg ggc gat tct aac gcg tct gtg ccc aca cct cag ccg gtt tat tac			2113
Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr			
690	695	700	

cgc gaa atg ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc 2161
 Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile

705

710

715

act ttt gtt tcc aaa gtc gcc tat gaa aat ggc gtg aaa gaa aaa cta 2209
 Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu

720

725

730

ggc tta gag cgc aag gtg cta ccc gtg aaa aac tgc cgc aac atc act 2257
 Gly Leu Glu Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr

735

740

745

aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat 2305
 Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp

750

755

760

765

cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2353
 Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys

770

775

780

ccc gcc tct gaa gtg cct cta gcc caa cgc tac act ttc ttc tag 2398
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785

790

795

gcacaat 2405

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<211> 226

<212> PRT

<213> Helicobacter felis

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1

5

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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln

20

25

30

FOET20-44000000

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
 35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
 50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
 65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
 210 215 220

Ile Lys

FOET 20-10000000

225

<210> 6

<211> 568

<212> PRT

<213> Helicobacter felis

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20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
145 150 155 160

FOR T20-7097050

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
 165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
 180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
 195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
 210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
 225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
 245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
 260 265 270

His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
 275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala

FOE F 40 = 42040000

355

360

365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
 435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
 450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
 465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
 485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
 500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
 515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
 530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
 545 550 555 560

TOEFTD=14640600

Leu Ala Gln Arg Tyr Thr Phe Phe
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<210> 7

<211> 2183

<212> DNA

<213> Helicobacter felis

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<221> CDS

<222> (3)..(683)

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<222> (694)..(2181)

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gcg ggc gaa gtg gct aga aag cgc aaa gca gag ggc tta aag ctc aat 95

Ala Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn

20 25 30

caa ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg 143

Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala

35 40 45

cgc cgt ggc aaa aaa acc gtt gct gaa ctt atg gaa gaa tgt atg cac 191

Arg Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His

50 55 60

ttt ttg aaa aaa gat gag gtg atg ccc ggt gtg ggg aat atg gtc cct 239

Phe Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro

65 70 75

FOR THE "HUBBARD"

Phe Ile Lys

225

Met Lys Met Lys Lys Gln Glu Tyr Val

230

235

aac acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc 768

Asn Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr

240

245

250

gat ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag 816

Asp Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu

255

260

265

ctc aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc 864

Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser

270

275

280

aat agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg 912

Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met

285

290

295

300

att atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat 960

Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn

305

310

315

ggc aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat 1008

Gly Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp

320

325

330

ggc gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca 1056

Gly Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala

335

340

345

ggg gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac 1104

Gly Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His

350

355

360

tto ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca 1152

Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr

365

370

375

380

acc atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc 1200
 Thr Met Phe Gly Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr
 385 390 395

acc atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct 1248
 Thr Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala
 400 405 410

gaa gag tat tct atg aat gta ggc ttt ttg ggc aaa ggc aat agt tct 1296
 Glu Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser
 415 420 425

agc aaa aaa caa ctt gta gaa caa gta gaa gcg ggc gcg att ggc ttt 1344
 Ser Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe
 430 435 440

aaa ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc 1392
 Lys Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys
 445 450 455 460

ttg agc gtg gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat 1440
 Leu Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp
 465 470 475

acg gtc aat gag gca ggt tat gtg gat gac acc cta aat gca atg aac 1488
 Thr Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn
 480 485 490

ggg cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac 1536
 Gly Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly Gly His
 495 500 505

tca cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc 1584
 Ser Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser
 510 515 520

tcc acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac 1632

Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His
 525 530 535 540

tta gac atg ctc atg acc tgc cac cac cta gat aag cgc atc cgc gag 1680
 Leu Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu
 545 550 555

gat tta caa ttt tct caa agc cgt atc cgc ccc gga tct att gcc gct 1728
 Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala
 560 565 570

gag gat gtg ctc cat gat att ggc gtg atc gcg atg act agc tcc gat 1776
 Glu Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp
 575 580 585

tcg caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa 1824
 Ser Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln
 590 595 600

act gca gat aag aat aaa gaa ttt ggt aag ctt cct gaa gat ggt 1872
 Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly
 605 610 615 620

gca gat aac gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc 1920
 Ala Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr
 625 630 635

att aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg 1968
 Ile Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val
 640 645 650

gaa gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt 2016
 Glu Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe
 655 660 665

ggc gtg aaa cct aag att gtg att aaa ggt ggc atg gtg gtc ttc tct 2064
 Gly Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser
 670 675 680

FOET-40-42400000

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val Thr
 115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
 165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
 195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
 210 215 220

Ile Lys
 225

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<213> Helicobacter felis

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TOE20-4600000

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Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr		
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Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile		
65	70	75 80
Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly		
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Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val		
100	105	110
Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr		
115	120	125
Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe		
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Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr		
145	150	155 160
Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp		
165	170	175
Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val		
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Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu		
195	200	205
Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly		
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Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
 225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
 245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
 260 265 270

His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
 275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
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His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430

FOET-1940-1940-1940

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
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 Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
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ttg aaa aaa gac gag gtg atg ccc ggt gtg ggg aat atg gtc cct gat 241
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 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
 85 90 95

aat tgg ccc atc gaa ccc gat gaa cac ttc aaa gcg ggc gaa gtc aaa 337
 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
 100 105 110

ttt ggc tgt gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc 385
 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
 115 120 125

gaa cta gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc 433
 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
 130 135 140

cat ttc cac ttc ttt gaa gcc aac aag gca ttg aaa ttc gat cgg gaa 481
 His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
 145 150 155 160

aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc 529
 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
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att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggc 577
 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
 180 185 190

Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly
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gaa ggt atg att att acc gct ggg ggg atc gat tca cac acc cac ttc 1106
 Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe
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 370 375 380

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 385 390 395

atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa 1250
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 Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser
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ttg cat gaa gac tgg ggc aca act cca agt gca atc gat cac tgc ttg 1394
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agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg 1442
 Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr
 465 470 475

gtc aat gag gca ggt tat gta gat gac acc ctg aat gcg atg aac ggg 1490
 Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly
 480 485 490

Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu
640 645 650

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Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly
655 660 665

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Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu
670 675 680 685

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Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr
690 695 700

cgc gaa atg ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc 2162
Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile
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Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu
720 725 730

ggc tta gag cgc aag gtg cta ccc gtg aaa aac tgc cgc aac atc act 2258
Gly Leu Glu Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr
735 740 745

aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat 2306
Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp
750 755 760 765

cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2354
Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys
770 775 780

ccc gcc tct gaa gtg cct cta gcc cag cgc tac act ttc ttc tag 2399
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2407

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Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
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Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu

145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
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Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
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Ile Lys
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Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

FOR THE "FOOD" FILE

275

280

285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
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Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
 435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
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Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
 465 470 475 480

FOE F 20 4 4840660

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
 485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
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Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
 515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
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Leu Ala Gln Arg Tyr Thr Phe Phe
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Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile
485 490 495

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His Ala Tyr His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val
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Ile Thr Met Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro
515 520 525

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530 535 540

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Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe
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Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu
565 570 575

cat gat atc ggt gtg atc gcg atg aca agt tcc gat tcg caa gca atg 1833
His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met
580 585 590

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Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys
595 600 605

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 625 630 635 640

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 Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys
 645 650 655

atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt ggc gta aaa ccc 2073
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 660 665 670

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 Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp
 675 680 685

tct aat gcg tct gtg ccc act cct cag ccg gtt tat tac cgc gaa atg 2169
 Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met
 690 695 700

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 Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val
 705 710 715 720

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 Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu
 725 730 735

cgc aag gtg ctc ccc gtg aaa aac tgc cgt aac atc acc aag aag gac 2313
 Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp
 740 745 750

ttc aag ttc aac gac aaa act gca aaa atc acc gtc gat ccg aaa acc 2361
 Phe Lys Phe Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr

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755

760

765

ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa ccc acc tct 2409

Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser

770

775

780

gaa gtg cct cta gcc caa cgc tac act ttc ttc tag gcataat

2452

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785

790

795

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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln

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25

30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg

35

40

45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe

50

55

60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp

65

70

75

80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val

85

90

95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys

100

105

110

FOET-10-1000000

FOET 20-1261060

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Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr		
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Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile		
65	70	75 80
Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly		
85	90	95
Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val		
100	105	110
Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr		
115	120	125
Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe		
130	135	140
Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr		
145	150	155 160
Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp		
165	170	175
Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val		
180	185	190
Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu		
195	200	205
Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly		
210	215	220
Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr		
225	230	235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
 245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
 260 265 270

His Ile Glu Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met
 275 280 285

Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
 290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
 305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
 325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
 340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
 355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
 370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
 385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
 405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
 420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
 435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
 450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
 465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
 485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
 500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
 515 520 525

Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
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